

## Comment

Factors embedded in health-care systems, stigma, and discrimination probably drive these consistent deficits. Solving these issues will need thoughtful application of best practices and additional research.<sup>5</sup>

Antiretroviral treatments for HIV have greatly improved with time, offering the promise of normal life expectancy for people living with HIV who successfully navigate the cascade. Yet, in North America, and around the world, losses from the various cascade steps can jeopardise the health outcomes of many people. Jurisdictions should develop metrics of care cascades and population-based assessments of HIV viral loads. Such data could provide a broad overview of the HIV treatment and prevention landscape and point to areas in need of improvement.

In this context, understanding the limiting factors in each of the cascade steps is important, with the recognition that what causes people to be lost from the cascade is likely to vary by region and individual. Although it is tempting to use cascades to compare countries, provinces, states, and other jurisdictions, differing HIV care guidelines, clinical practice, data reporting, and data availability make such comparisons difficult. Instead, the value of the cascade lies in its ability to guide local programmes and jurisdictions to address problematic cascade transitions.

By following the cascade over time, jurisdictions can assess the effectiveness of programmes and interventions. Nosyk and colleagues' study is an

excellent example of the usefulness of reviewing cascades of care over time—we look forward to seeing more studies of this kind in the future. Shared successes will hopefully help the global HIV community to improve care worldwide.

Edward M Gardner, \*Benjamin Young

Denver Public Health, Denver, CO, USA (EMG); Division of Infectious Diseases, Department of Medicine, University of Colorado Denver, Aurora, CO, USA (EMG); International Association of Providers of AIDS Care, Washington, DC 20005, USA (BY); and Josef Korbel School of International Studies, University of Denver, Denver, CO, USA (BY)  
byoung@iapac.org

EMG declares that he has no conflicts of interest. BY has received consulting or speaking fees from Bristol-Myers Squibb, Cerner Corporation, Gilead Sciences, GlaxoSmithKline, Merck, Monogram Biosciences, and ViiV Healthcare; and has received research funding from Gilead Sciences, GlaxoSmithKline, Merck, and ViiV Healthcare.

- 1 Gardner, EM, McLees MP, Steiner JF, et al. The spectrum of engagement in HIV care and its relevance to test-and-treat strategies for prevention of HIV infection. *Clin Infect Dis* 2011; **52**: 793–800.
- 2 Nosyk B, Montaner JSG, Colley G, et al, for the STOP HIV/AIDS Study Group. The cascade of HIV care in British Columbia, Canada, 1996–2011: a population-based retrospective cohort study. *Lancet Infect Dis* 2013; published online Sept 27. [http://dx.doi.org/10.1016/S1473-3099\(13\)70254-8](http://dx.doi.org/10.1016/S1473-3099(13)70254-8).
- 3 Gardner, EM, Daniloff E, Thrun MW, et al. Initial linkage and subsequent retention in HIV care for a newly diagnosed HIV-infected cohort in Denver, Colorado. *J Int Assoc Provid AIDS Care* 2013; published online Aug 20. DOI:10.1177/2325957413500532.
- 4 Cohen SM, Van Handel MM, Branson BM, et al. Vital signs: HIV prevention through care and treatment—United States. *MMWR Morb Mortal Wkly Rep* 2011; **60**: 1618–23.
- 5 Thompson MA, Mugavero MJ, Amico KR, et al., Guidelines for improving entry into and retention in care and antiretroviral adherence for persons with HIV: evidence-based recommendations from an International Association of Physicians in AIDS Care panel. *Ann Intern Med* 2012; **156**: 817–33.



## The epidemiology of MERS-CoV

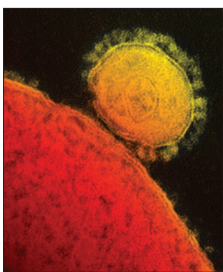
"The oldest and strongest emotion of mankind is fear, and the oldest and strongest kind of fear is fear of the unknown"

Howard Phillips Lovecraft

Coping with, and trying to understand, emerging epidemics has been part of the human experience since time immemorial. The concern that attends the emergence of a novel infectious disease might be substantial, but fears often subside as the disease becomes better understood, partly because initial findings tend to be biased towards cases and case clusters with more severe outcomes.<sup>1–3</sup> Epidemiologists and microbiologists are currently working to better characterise the outbreak of Middle Eastern respiratory

syndrome (MERS) coronavirus infection that made its initial appearance in a health-care-based outbreak in Jordan in 2012.<sup>4</sup> The understanding of the natural history and epidemiology of an emerging infectious disease allows us to predict its behaviour and identify control strategies. In *The Lancet Infectious Diseases*, the study by Simon Cauchemez and colleagues<sup>5</sup> is timely and important, since it provides us with such information about the emerging MERS outbreak.

We were impressed by the extent to which Cauchemez and co-authors did their analyses using limited publicly available data. Whereas decision makers often ask infectious disease modellers to provide an epidemiological crystal ball that shows what will happen,



Published Online

November 13, 2013

[http://dx.doi.org/10.1016/S1473-3099\(13\)70283-4](http://dx.doi.org/10.1016/S1473-3099(13)70283-4)

See [Articles](#) page 50

Copyright © Fisman et al. Open Access article distributed under the terms of CC BY-NC-ND

these investigators use modelling more appropriately, as a method for the quantification and management of uncertainty. What does their analysis tell us?

A key epidemiological parameter early in an emerging epidemic is the basic reproductive number ( $R_0$ ), which describes the average number of new cases of infection generated by one primary case in a susceptible population.<sup>6</sup>  $R_0$  affects the growth rate of an outbreak and the total number of people infected by the end of the outbreak. When  $R_0$  is lower than 1, a sustained epidemic will not occur. Using epidemiological and genetic data, the authors estimated that  $R_0$  was small (consistent with earlier estimates),<sup>7,8</sup> but might be slightly greater than 1. However,  $R_0$  estimates based on disease cluster sizes were lower than 1, suggesting that cluster identification leads to application of successful control measures. Using data on MERS-infected travellers returning from the Middle East, the investigators estimated MERS incidence, and back-calculated the likely extent of case underreporting; they estimated that most cases have been undetected.

These findings suggest that mildly symptomatic cases are common, with implications for the effectiveness of infection control measures. They also show us that the MERS outbreak represents a dynamic process, with human incidence possibly portraying transmission from animal to man occurring in the context of an as yet unconfirmed epizootic.

The distance between the raw, publicly available, epidemiological and virological data obtained by the authors, and the insights provided by them in their report can represent the distance between abundant information and actionable knowledge. The quality of data available to these authors is poor, but should that have prevented them from proceeding with analysis until better data were available? We do not think so: inferences based on the best available data, even if those data are imperfect, allow decision makers to follow optimum courses of action based on what is known at a given point in time. Could the estimates presented here be refined if more complete data were to become available? Undoubtedly, and it seems likely that these investigators and others will continue to do so as this disease is further studied.

The widespread, transparent, and trans-jurisdictional sharing of epidemiological data in the context of

public health emergencies could improve the accuracy of early efforts at epidemiological synthesis, such as those presented here by Cauchemez and colleagues.<sup>5</sup> However, many disincentives for such sharing by jurisdictions experiencing outbreaks remain, including lost travel and tourism, concerns about data security, and interest in scientific publication. Creative epidemiologists and computer scientists have shown various means to infer levels of disease activity with indirect Internet data mining techniques.<sup>9–11</sup> The ability to draw inferences about diseases from non-traditional data sources will hopefully both provide alternate means of characterising epidemics, and diminish the temptation towards non-transparency in traditional public health authorities. The resultant improvements in rapid epidemiological risk estimates would benefit all of us.

\*David N Fisman, Ashleigh R Tuite

Dalla Lana School of Public Health, University of Toronto,  
155 College Street, Room 586, Toronto, ON M5T 3M7, Canada  
(DNF, ART)

david.fisman@utoronto.ca

We declare that we have no conflicts of interest.

- 1 Presanis AM, De Angelis D, New York City Swine Flu Investigation Team, et al. The severity of pandemic H1N1 influenza in the United States, from April to July 2009: a Bayesian analysis. *PLoS Med* 2009; **6**: e1000207.
- 2 Yu H, Cowling BJ, Feng L, et al. Human infection with avian influenza A H7N9 virus: an assessment of clinical severity. *Lancet* 2013; **382**: 138–45.
- 3 Penttinen P, Kaasik-Aasav K, Friaux A, et al. Taking stock of the first 133 MERS coronavirus cases globally—Is the epidemic changing? *Euro Surveill* 2013; **18**: 20596.
- 4 European Centre for Disease Prevention and Control. Severe respiratory disease associated with Middle East respiratory syndrome coronavirus (MERS-CoV). Updated rapid risk assessment, 7th update. Stockholm: European Centre for Disease Prevention and Control, 2013. [http://www.ecdc.europa.eu/en/publications/Publications/RRA\\_MERS-CoV\\_7th\\_update.pdf](http://www.ecdc.europa.eu/en/publications/Publications/RRA_MERS-CoV_7th_update.pdf) (accessed Oct 22, 2013).
- 5 Cauchemez S, Fraser C, Van Kerkhove MD, et al. Middle East respiratory syndrome coronavirus: quantification of the extent of the epidemic, surveillance biases, and transmissibility. *Lancet Infect Dis* 2013; published online Nov 13. [http://dx.doi.org/10.1016/S1473-3099\(13\)70304-9](http://dx.doi.org/10.1016/S1473-3099(13)70304-9).
- 6 Pandemic Influenza Outbreak Research Modelling Team, Fisman T. Modelling an influenza pandemic: a guide for the perplexed. *CMAJ* 2009; **181**: 171–73.
- 7 Breban R, Riou J, Fontanet A. Interhuman transmissibility of Middle East respiratory syndrome coronavirus: estimation of pandemic risk. *Lancet* 2013; **382**: 694–99.
- 8 ProMED Mail, PRO/AH/EDR> MERS-CoV - Eastern Mediterranean (11): Saudi Arabia, new death. [4] Transmissibility and cluster sizes. ProMED-mail 2013; May 27: 20130527.1738597. <http://www.promedmail.org>. (accessed Sept 7, 2013).
- 9 Brownstein JS, Freifeld CC. HealthMap: the development of automated real-time internet surveillance for epidemic intelligence. *Euro Surveill* 2007; **12**: E0711295.
- 10 St Louis C, Zorlu G. Can Twitter predict disease outbreaks? *BMJ* 2012; **344**: e2353.
- 11 Ginsberg J, Mohebbi MH, Patel RS, Brammer L, Smolinski MS, Brilliant L. Detecting influenza epidemics using search engine query data. *Nature* 2009; **457**: 1012–14.